



24577-cyb.ST25
SEQUENCE LISTING

<110> Maddon, Paul J.

<120> DERIVATIVES OF SOLUBLE T-4

<130> 24577-CY-B

<140> 09/891,119

<141> 2001-06-25

<160> 22

<170> PatentIn version 3.1

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gtg ctg caa ctg cgc ctc ctc cca gca gcc act cag gga aag aaa gtg Val Leu Gln Leu Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val		159																
15																		
gtg ctg ggc aaa aaa ggg gat aca gtg gaa ctg acc tgt aca gct tcc Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser		207																
30																		
cag aag aag agc ata caa ttc cac tgg aaa aac tcc aac cag ata aag Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys		255																
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att ctg gga aat cag ggc tcc tcc tta act aaa ggt cca tcc aag ctg Ile Leu Gly Asn Gln Gly Ser Ser Leu Thr Lys Gly Pro Ser Lys Leu		303																
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aat gat cgc gct gac tca aga aga agc ctt tgg gac caa gga aac ttc Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe		351																
80																		
85																		
ccc ctg atc atc agg aat ctt aag ata gaa gac tca gat act tac atc Pro Leu Ile Ile Arg Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile		399																
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ttg act gcc aac tct gac acc cac ctg ctt cag ggg cag agc ctg acc Leu Thr Ala Asn Ser Asp Thr His Ser Leu Leu Gln Gly Ser Leu Thr		495																
125																		
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145																		
150																		
agt cca agg ggt aaa aac ata cag ggg ggg aag acc ctc tcc gtg tct Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser		591																
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165																		
cag ctg gag ctc cag gat agt ggc acc tgg aca tgc act gtc ttg cag Gln Lys Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln		639																
175																		
180																		
aac cag aag aag gtg gag ttc aaa ata gac atc gtg gtg cta gct ttc Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe		687																
190																		
205																		
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210																		
225																		
230																		
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acc ttt gac ctg aag aac aag gaa gtg tct gta aaa cgg gtt acc cag 879
 Thr Phe Asp Leu Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln
 255 260 265
 gac cct aag ctc cag atg ggc aag aag ctc cgg ctc cac ctc acc ctg 927
 Asp Pro Lys Leu Gln Met Gly Lys Lys Leu Pro Leu His Leu Thr Leu
 270 275 280
 ccc cag gcc ttg cct cag tat gct ggc tct gga aac ctc acc ctg gcc 975
 Pro Gln Ala Leu Pro Gln Tyr Ala Gly Ser Gly Asn Leu Thr Leu Ala
 285 290 295 300
 ctt gaa gcg aaa aca gga aag ttg cat cag gaa gtg aac ctc gtg gtg 1023
 Leu Glu Ala Lys Thr Gly Lys Leu His Gln Glu Val Asn Leu Val Val
 305 310 315
 atg aga gcc act cag ctc cag aaa aat ttg acc tgt gag gtg tgg gga 1071
 Met Arg Ala Thr Thr Gln Lys Asn Leu Thr Cys Glu Val Trp Gly
 320 325 330
 ccc acc tcc cct aag ctg atg ctg agc ttg aaa ctg gag aac aag gag 1119
 Pro Thr Ser Pro Lys Leu Met Leu Ser Leu Lys Leu Asn Lys Glu
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 gca aag gtc tcg aag cgg gag aag gcg gtg tgg gtg ctg aac cct gag 1167
 Ala Lys Val Ser Lys Arg Glu Lys Ala Val Trp Val Leu Asn Pro Glu
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 gcg ggg atg tgg cag tgt ctg ctg agt gac tcg gga cag gtc ctg ctg 1215
 Ala Gly Met Trp Gln Cys Leu Leu Ser Asp Ser Gly Gln Val Leu Leu
 365 370 375 380
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Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
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35

40

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 Gln Gly Ser Ser Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
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 Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
 85 90 95
 Arg Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu
 100 105 110
 Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
 115 120 125
 Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu
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 Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
 145 150 155 160
 Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
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 Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys
 180 185 190
 Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Gln Lys Ala Ser
 195 200 205
 Ser Ile Val Tyr Lys Lys Glu Gly Glu Gln Val Asp Phe Ser Phe Pro
 210 215 220
 Leu Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly Glu Leu Trp Trp
 225 230 235 240
 Gln Ala Glu Arg Ala Ser Ser Ser Lys Ser Trp Ile Thr Phe Asp Leu
 245 250 255
 Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln Asp Pro Lys Leu
 260 265 270
 Gln Met Gly Lys Lys Leu Pro Leu His Leu Thr Leu Pro Gln Ala Leu
 275 280 285

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Pro Gln Tyr Ala Gly Ser Gly Asn Leu Thr Leu Ala Leu Glu Ala Lys
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Thr Gly Lys Leu His Gln Glu Val Asn Leu Val Val Met Arg Ala Thr
305 310 315 320

Gln Leu Gln Lys Asn Leu Thr Cys Glu Val Trp Gly Pro Thr Ser Pro
325 330 335

Lys Leu Met Leu Ser Leu Lys Leu Glu Asn Lys Glu Ala Lys Val Ser
340 345 350

Lys Arg Glu Lys Ala Val Trp Val Leu Asn Pro Glu Ala Gly Met Trp
355 360 365

Gln Cys Leu Leu Ser Asp Ser Gly Gln Val Leu Leu Glu Ser Asn Ile
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Lys Val Leu Pro Thr Trp Ser Thr Pro Val Trp Arg Leu
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<213> Artificial Sequence

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 ggcgagctgt ggtggcaggc ggagagggtc tctcctcca agtcttgat cactttgac 840
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35 40 45

Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn
50 55 60

Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
65 70 75 80

Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
85 90 95

Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu
100 105 110

Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
115 120 125

Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu
130 135 140

Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
145 150 155 160

Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
165 170 175

Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys
180 185 190

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val Glu Phe Lys Ile Asp Ile val val Leu Ala Phe Gln Lys Ala Ser
 195 200 205

Ser Ile Val Tyr Lys Lys Glu Gly Glu Gln Val Glu Phe Ser Phe Pro
 210 215 220

Leu Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly Glu Leu Trp Trp
 225 230 235 240

Gln Ala Glu Arg Ala Ser Ser Ser Lys Ser Trp Ile Thr Phe Asp Leu
 245 250 255

Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln Asp Pro Lys Leu
 260 265 270

Gln Met Gly Lys Lys Leu Pro Leu His Leu Thr Leu Pro Gln Ala Leu
 275 280 285

Pro Gln Tyr Ala Gly Ser Gly Asn Leu Thr Leu Ala Leu Glu Ala Lys
 290 295 300

Thr Gly Lys Leu His Gln Glu Val Asn Leu Val Val Met Arg Ala Thr
 305 310 315 320

Gln Leu Gln Lys Asn Leu Thr Cys Glu Val Trp Gly Pro Thr Ser Pro
 325 330 335

Lys Leu Met Leu Ser Leu Lys Leu Glu Asn Lys Glu Ala Lys Val Ser
 340 345 350

Lys Arg Glu Lys Ala Val Trp Val Leu Asn Pro Glu Ala Gly Met Trp
 355 360 365

Gln Cys Leu Leu Ser Asp Ser Gly Gln Val Leu Leu Glu Ser Asn Ile
 370 375 380

Lys Val Leu Pro Thr Trp Ser Thr Pro Val Gln Pro Met Ala Leu Ile
 385 390 395 400

Val Leu Gly Gly Val Ala Gly Leu Leu Leu Phe Ile Gly Leu Gly Ile
 405 410 415

Phe Phe Cys Val Arg Cys Arg His Arg Arg Arg Gln Ala Glu Arg Met
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His Arg Phe Gln Lys Thr Cys Ser Pro
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Thr Cys Thr Ala Ser Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn
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Ser Asn Gln Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys
 35 40 45

Gly Pro Ser Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp
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Asp Gln Gly Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp
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Ser Asp Thr Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu
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Asp Ile Val Thr Met Thr Cys Gln Ala Ser Gln Gly Thr Ser Ile Asn
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Leu Asn Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Gly Ala ser Ile Leu Glu Asp Gly Val Pro Ser Arg Phe ser Gly
50 55 60

Ser Arg Tyr Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Asp
65 70 75 80

Glu Asp Met Ala Thr Tyr Phe Cys Leu Gln His Ser Tyr Leu Pro Tyr
85 90 95

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Thr Gly Cys Trp Ile Gly Arg Phe Gly Ser Leu Ile Tyr Cys
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<210> 13

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1 5 10 15

Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser Asn Pro Thr Ser Gly
20 25 30

Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala Ala Ser Pro Thr Phe
35 40 45

Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala Ala Glu Gly Leu Asp
50 55 60

Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp Thr Phe Val Leu Thr
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Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr Tyr Phe Cys Ser Ala
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Leu Ser Asn Ser Ile Met
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<211> 102

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Asp Ala Gly Val Ile Gln Ser Pro Arg His Glu Val Thr Glu Met Gly
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Gln Glu Val Thr Leu Arg Cys Lys Pro Ile Ser Gly His Asn Ser Leu
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Phe Trp Tyr Arg Gln Thr Met Met Arg Gly Leu Glu Leu Ile Tyr
35 40 45

Phe Asn Asn Asn Val Pro Ile Asp Asp Ser Gly Met Pro Glu Asp Arg
50 55 60

Phe Ser Ala Lys Met Pro Asn Ala Ser Phe Ser Thr Leu Lys Ile Gln
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Pro Ser Glu Pro Arg Asp Ser Ala Val Tyr Phe Cys Ala Ser Ser Phe
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Ser Thr Cys Ser Ala Asn
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Leu Phe Trp Tyr Lys Gln Pro Pro Ser Gly Glu Leu Val Phe Leu Ile
 35 40 45

Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu Ile Ser Gly Arg Tyr Ser
 50 55 60

Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn Phe Thr Ile Thr Ala
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Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys Ala Leu Asp Ser Ser
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Ala Ser Lys

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Leu Gly Leu Leu Phe Leu Gly Leu Gly Leu Phe Ile Tyr Phe Arg
20 25 30



Figure 6A

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				L	
				+10	
				* leu val leu gln leu ala leu leu pro ala ala thr gln gly lys val leu gln lys gln val leu gln leu thr cys	
				CTG GTG CTA CAA CTG GGG CTC CTC CCA GGC ACT CAG GGA MAG AAA GTG GTG GCA GAT ACA GTG GAA CTG ACC TGT 198	
				V1	
				+40	
				thr ala ser gln lys lys ser ile gln phe his trp lys asn ser asn gln ile lys ile leu gln gln gly ser phe leu thr lys	
				ACA CTT TCC CAG CAG MAG AGC ACA CAA TTC CAC TCA TCG TGG AAA ACC TCC MAC CAG ACA MAG ATT CTG GCA ATT CAG GGC TCC TTC TTA ACT AAA 288	
				+70	
				gly pro ser lys leu asn asp arg ala asp ser arg arg ser leu trp asp gln gly asn phe pro leu ile ile lys asn leu lys ile	
				GGT CCA TCC MAG CTC AAT GAT CAC CTT CAC TCA ACA ACA ACC CTT TCG CAC CAA GCA AAC TTC CCC CTG ATC ATC ATC ANG ATT CTT ANG ACA 378	
				+100	
				gln asp ser asp thr tyr ile cys gln val gln asp gln lys gln gln val gln leu leu val phe gly leu thr ala asn ser asp thr	
				GAA GAC TCA CAA GAT ACT TAC ATC TGT GAA GTG CAG GAC CAG MAG CAG CAG GAG CAA TTG CTA GTG TTC GCA TTG ACT GGC AAC TCT GAC ACC 468	
				V1	
				+120	
				his leu leu gln gly gln ser leu thr leu thr leu gln ser pro pro gly ser ser pro ser val gln cys arg ser pro arg gly lys	
				CAC CTG CTT CAG GGG CAG MAG ACC CTG ACC CTG ACC TTG CAG ACC CCC CTT GGT AGT ACC CCC TCA GTG CAA TGT AGG AGT CCA AGG GGT AAA 558	
				V2	
				+150	
				asn ile gln gly gly lys thr leu ser val ser gln leu gln leu gln asp ser gly thr trp thr cys thr val leu gln asn gln lys	
				AAC ACA CAG GGG GGG MAG ACC CTC TCC GTG TGT CAG CTC CAG CTC CAG GAT AGT GGC ACC TCG ACA TCT ACT GTC TTG CAG AAC 648	
				V2	
				+180	
				lys val gln phe lys ile asp ile val val leu ala phe gln lys ala ser ile val tyr lys lys gln gly gln val gln phe	
				NAG GTG GAG TTC AAA ATA CAC ATC CAC ATC CTT TTC CAG MAG GGC TCC ACC ACA GTC TAT MAG AAA GAG GGG GAA CAG GTG GAG TTC 738	
				V3	
				+220	
				ser phe pro leu ala phe thr val gln lys leu thr gly ser gly gln leu trp trp gln ala gln arg ala ser ser lys ser trp	
				TCC TTC CCA CTC CCC TTT ACA GTT GAA MAG CTG AGC GGC AGT GGC CAG CTC TCG TCG CAG GGG MAG GGC CTT TCC TCC ANG TCT TCG 828	

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CCATGTTCTCTCCTGGTTCAGCGGCGGACCACTGC

CCTCATTAATTTCTGTCTGACCCCTCCTGCCACTCTCAATTTCAGTACC 1742

Figure 6B

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00NATGHTTCTTC7CGGTTCAGCCCCCCTWCACGTCTCAGTGTTCCCTCTCTACTGTTTCGACGGTTCATCTCACCGGTCTCTGCACGCCCATTTCTTTTCTTCATGACGCTTCACGCTTCTTCT 1697

CTCATTTATTTCTCTCTGAGCCCTCTCCGACCTGCTCATTTGGATCC 1742